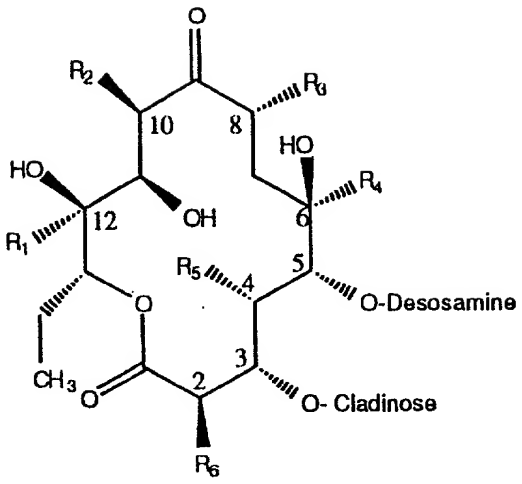
What is claimed is:

1. A compound of the formula:



X

wherein

R_1, R_2, R_3, R_4, R_5, and R_6 are independently selected from Q wherein Q is selected from the group consisting of (a) -H, (b) -Me, (c) -Et, and (d) -OH;

L_1 and L_2 are independently -H or -OH;

L_3 is D-desosamine or -OH; and

L_4 is L-mycarose, L-cladinose or -OH

with the proviso that when R_1-R_5 are -Me, R_6 is other than -H or -Me.

2. The compound of claim 1 wherein Q is selected from the group consisting of (a), (b), and (c) and L_1, L_2, L_3 and L_4 are as defined therein.

3. The compound of claim 1 wherein Q is selected from the group consisting of (a), (b), and (d) and L_1, L_2, L_3 and L_4 are as defined therein.

4. The compound of claim 1 wherein Q is selected from the group consisting of (a), (c), and (d) and L_1, L_2, L_3 and L_4 are as defined therein.

5. The compound of claim 1 wherein Q is selected from the group consisting of (b), (c), and (d) and L_1, L_2, L_3 and L_4 are as defined therein.

6. The compound of claim 1 wherein Q is selected from the group consisting of (a) and (b) and L_1, L_2, L_3 and L_4 are as defined therein.

7. The compound of claim 1 wherein Q is selected from the group consisting of (a) and (c) and L_1, L_2, L_3 and L_4 are as defined therein.

8. The compound of claim 1 wherein Q is selected from the group consisting of (a) and (d) and L_1, L_2, L_3 and L_4 are as defined therein.

9. The compound of claim 1 wherein Q is selected from the group consisting of (b) and (c) and L_1, L_2, L_3 and L_4 are as defined therein.

10. The compound of claim 1 wherein Q is selected from the group consisting of (b) and (d) and L_1, L_2, L_3 and L_4 are as defined therein.

11. The compound of claim 1 wherein Q is selected from the group consisting of (c) and (d) and L_1, L_2, L_3 and L_4 are as defined therein.

12. The compound of claim 1 wherein Q is (a) and L_1, L_2, L_3 and L_4 are as defined therein.

13. The compound of claim 1 wherein Q is (c) and L_1, L_2, L_3 and L_4 are as defined therein.

14. The compound of claim 1 wherein Q is (d) and L_1, L_2, L_3 and L_4 are as defined therein.

15. The compound of claim 1 wherein

(a) R_6 and R_1 are -H and R_2, R_3, R_4 and R_5 are -Me,
(b) R_5 and R_1 are -H and R_2, R_3, R_4 and R_6 are -Me,
(c) R_4 and R_1 are -H and R_2, R_3, R_5 and R_6 are -Me,
(d) R_3 and R_1 are -H and R_2, R_4, R_5 and R_6 are -Me,
(e) R_2 and R_1 are -H and R_3, R_4, R_5 and R_6 are -Me,
(f) R_6 and R_2 are -H and R_1, R_3, R_4 and R_5 are -Me,
(g) R_5 and R_2 are -H and R_1, R_3, R_4 and R_6 are -Me,
(h) R_4 and R_2 are -H and R_1, R_3, R_5 and R_6 are -Me,
(i) R_3 and R_2 are -H and R_1, R_4, R_5 and R_6 are -Me,
(j) R_6 and R_3 are -H and R_1, R_2, R_4 and R_5 are -Me,
(k) R_5 and R_3 are -H and R_1, R_2, R_4 and R_6 are -Me,
(l) R_4 and R_3 are -H and R_1, R_2, R_5 and R_6 are -Me,

(m) R_6 and R_4 are -H and R_1, R_2, R_3 and R_5 are -Me,

(n) R_5 and R_4 are -H and R_1, R_2, R_3 and R_6 are -Me,

(o) R_6 and R_5 are -H and R_1, R_2, R_3 and R_4 are -Me, and

L_1, L_2, L_3 and L_4 are as defined therein.

16. The compound of claim 15 wherein (a)-(o) are as defined therein, L_1 and L_2 are -OH, L_3 is D-desosamine and L_4 is L-cladinose.

17. The compound of claim 1 wherein

(a) R_6, R_2 and R_1 are -H and R_3, R_4 and R_5 are -Me,

(b) R_5, R_2 and R_1 are -H and R_3, R_4 and R_6 are -Me,

(c) R_4, R_2 and R_1 are -H and R_3, R_5 and R_6 are -Me,

(d) R_3, R_2 and R_1 are -H and R_4, R_5 and R_6 are -Me,

(e) R_6, R_3 and R_1 are -H and R_2, R_4 and R_5 are -Me,

(f) R_5, R_3 and R_1 are -H and R_2, R_4 and R_6 are -Me,

(g) R_4, R_3 and R_1 are -H and R_2, R_5 and R_6 are -Me,

(h) R_6, R_4 and R_1 are -H and R_2, R_3 and R_5 are -Me,

(i) R_5, R_4 and R_1 are -H and R_2, R_3 and R_6 are -Me,

(j) R_6, R_5 and R_1 are -H and R_2, R_3 and R_4 are -Me,

(k) R_6, R_3 and R_2 are -H and R_1, R_4 and R_5 are -Me,

(l) R_5, R_3 and R_2 are -H and R_1, R_4 and R_6 are -Me,

(m) R_4, R_3 and R_2 are -H and R_1, R_5 and R_6 are -Me,

(n) R_6, R_4 and R_2 are -H and R_1, R_3 and R_5 are -Me,

(o) R_5, R_4 and R_2 are -H and R_1, R_3 and R_6 are -Me,

(p) R_6, R_5 and R_2 are -H and R_1, R_3 and R_4 are -Me,

(q) R_6, R_4 and R_3 are -H and R_1, R_2 and R_5 are -Me,

(r) R_5, R_4 and R_3 are -H and R_1, R_2 and R_6 are -Me,

(s) R_6, R_5 and R_3 are -H and R_1, R_2 and R_4 are -Me, or

(t) R_6, R_5 and R_4 are -H and R_1, R_2 and R_3 are -Me, and

L_1, L_2, L_3 and L_4 are as defined therein.

18. The compound of claim 17 wherein (a)-(t) are as defined therein, L_1 and L_2 are -OH, L_3 is D-desosamine and L_4 is L-cladinose.

19. The compound of claim 1 wherein

(a) R_6, R_3, R_2 and R_1 are -H and R_5, and R_4 are -Me,

(b) R_5, R_3, R_2 and R_1 are -H and R_6, and R_4 are -Me,

(c) R_4, R_3, R_2 and R_1 are -H and R_5, and R_6 are -Me,

(d) R_6, R_4, R_2 and R_1 are -H and R_3, and R_5 are -Me,
(e) R_5, R_4, R_2 and R_1 are -H and R_3, and R_6 are -Me,
(f) R_6, R_5, R_2 and R_1 are -H and R_3, and R_4 are -Me,
(g) R_6, R_4, R_3 and R_1 are -H and R_2, and R_5 are -Me,
(h) R_5, R_4, R_3 and R_1 are -H and R_2, and R_6 are -Me,
(i) R_6, R_5, R_4 and R_1 are -H and R_2, and R_3 are -Me,
(j) R_2, R_4, R_3 and R_1 are -H and R_5, and R_6 are -Me,
(k) R_6, R_4, R_3 and R_2 are -H and R_1, and R_5 are -Me,
(l) R_5, R_4, R_3 and R_2 are -H and R_1, and R_6 are -Me,
(m) R_6, R_5, R_3 and R_2 are -H and R_1, and R_4 are -Me, or
(n) R_6, R_5, R_4 and R_3 are -H and R_1, and R_2 are -Me, and

L_1, L_2, L_3 and L_4 are as defined therein.

20. The compound of claim 19 wherein (a)-(n) are as defined therein, L_1 and L_2 are -OH, L_3 is D-desosamine and L_4 is L-cladinose.

21. The compound of claim 1 wherein

(a) R_5, R_4, R_3, R_2 and R_1 are -H and R_6 is -Me,
(b) R_6, R_4, R_3, R_2 and R_1 are -H and R_5 is -Me,
(c) R_6, R_5, R_3, R_2 and R_1 are -H and R_4 is -Me,
(d) R_6, R_5, R_4, R_2 and R_1 are -H and R_3 is -Me,
(e) R_6, R_5, R_4, R_3 and R_1 are -H and R_2 is -Me, or
(f) R_6, R_5, R_4, R_3 and R_2 are -H and R_1 is -Me, and

L_1, L_2, L_3 and L_4 are as defined therein.

22. The compound of claim 21 wherein (a)-(f) are as defined therein, L_1 and L_2 are -OH, L_3 is D-desosamine and L_4 is L-cladinose.

23. The compound of claim 1 wherein R_1, R_2, R_3, R_4, R_5 and R_6 are -H and L_1, L_2, L_3 and L_4 are as defined therein.

24. The compound of claim 23 wherein R_1, R_2, R_3, R_4, R_5 and R_6 are as defined therein, L_1 and L_2 are -OH, L_3 is D-desosamine and L_4 is L-cladinose.

25. The compound of claim 1 selected from the group consisting of 6,10-didesmethyl-6-ethylerythromycin A; 10,12-didesmethyl-12-deoxy-12-ethylerythromycin A; 10,12-didesmethyl-12-deoxy-10-hydroxyerythromycin A; 6,10,12-tridesmethyl-6,12-diethylerythromycin A, and 6,10,12-tridesmethyl-6-deoxy-6,12-diethylerythromycin A.

26. The compound of claim 1 selected from the group consisting of 10-desmethylerythronolide B, 10-desmethyl-6-deoxyerythronolide B, 12-desmethylerythronolide B, 12-desmethyl-6-deoxyerythronolide B, 12-desmethyl-12-ethylerythronolide B, 6-desmethyl-6-deoxy-6-ethylerythronolide B, 10-desmethylerythromycin A, 10-desmethyl-12-deoxyerythromycin A, 10-desmethyl-6,12-dideoxyerythromycin A, 12-desmethylerythromycin A, 12-desmethyl-12-deoxyerythromycin A, 12-desmethyl-6,12-dideoxyerythromycin A, 6-desmethyl-6-ethylerythromycin A, 12-desmethyl-12-ethylerythromycin A, 12-desmethyl-12-deoxy-12-ethylerythromycin A, 10-desmethyl-10-hydroxyerythromycin A, 12-desmethyl-12-epihydroxyerythromycin A, 10,12-didesmethylerythromycin A, 10,12-didesmethyl-12-deoxyerythromycin A, and 10,12-didesmethyl-6,12-dideoxyerythromycin A.

27. The compound of claim 1 selected from the group consisting of 10-desmethylerythronolide B, 10-desmethyl-6-deoxyerythronolide B, 12-desmethylerythronolide B, 12-desmethyl-6-deoxyerythronolide B, 10-desmethylerythromycin A, 10-desmethyl-12-deoxyerythromycin A, 10-desmethyl-6,12-dideoxyerythromycin A, 12-desmethylerythromycin A, 12-desmethyl-12-deoxyerythromycin A, 12-desmethyl-6,12-dideoxyerythromycin A, 10,12-didesmethylerythromycin A, 10,12-didesmethyl-12-deoxyerythromycin A, and 10,12-didesmethyl-6,12-dideoxyerythromycin A.

28. A compound selected from the group consisting of 10-desmethylerythromycin A, 10-desmethyl-12-deoxyerythromycin A, and 12-desmethyl-12-deoxyerythromycin A.

29. An isolated polynucleotide sequence or fragment thereof which encodes an enzymatically active acyltransferase domain from a polyketide-producing microorganism selected from the group consisting of *Streptomyces hygroscopicus*, *Streptomyces venezuelae*, and *Streptomyces caelestis*.

30. The polynucleotide of Claim 29 selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:29 and SEQ ID NO:30.

31. The polynucleotide of Claim 29 wherein said acyltransferase domain is selected from the group consisting of SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33 and SEQ ID NO:34.

32. A vector comprising a polynucleotide sequence or fragment thereof which encodes an enzymatically active acyltransferase domain from *Streptomyces*.

33. The vector of Claim 32 wherein said *Streptomyces* is selected from the group consisting of *Streptomyces hygroscopicus*, *Streptomyces venezuelae*, and *Streptomyces caelestis*.

34. The vector of Claim 32 which is pCS5.

35. The vector of Claim 32 wherein said polynucleotide is selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:29 and SEQ ID NO:30.

36. The vector of Claim 32 wherein said acyltransferase domain is selected from the group consisting of SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33 and SEQ ID NO:34.

37. A vector selected from the group consisting of pUC18/LigAT2, pEryAT1/LigAT2, pEryAT2/LigAT2, pUC18/venAT, pEryAT1/venAT, pUC19/rapAT14, pEryAT1/rapAT14, pEryAT2/rapAT14, pUC/5'-flank/ethAT, pUC/ethAT/C-6, pEAT4, pUC18/NidAT6, and pEryAT2/NidAT6.

38. A host cell transformed with the vector of Claim 32.

39. The host cell of Claim 38 wherein said cell is a bacterial cell.

40. The host cell of Claim 39 wherein said bacterial cell is selected from the group consisting of *E. coli* and *Bacillus* species.

41. The host cell of Claim 40 wherein said cell is a polyketide-producing microorganism.

42. The host cell of Claim 41 wherein said polyketide-producing microorganism is selected from the group consisting of *Saccharopolyspora* species, *Nocardia* species, *Micromonospora* species, *Arthrobacter* species, *Streptomyces* species, *Actinomadura* species, and*Dactylosporangium*. species.

43. The host cell of Claim 42 wherein said polyketide-producing microorganism is selected from the group consisting of *Saccharopolyspora hirsuta, Micromonospora rosaria, Micromonospora megalomicea, Streptomyces antibioticus, Streptomyces mycarofaciens, Streptomyces avermitilis, Streptomyces hygroscopicus, Streptomyces caelestis, Streptomyces tsukubaensis, Streptomyces fradiae, Streptomyces platensis, Streptomyces violaceoniger, Streptomyces ambofaciens, Streptomyces griseoplanus*, and *Streptomyces venezuelae*.

44. The host cell of Claim 42 wherein said polyketide-producing microorganism is selected from the group consisting of *Saccharopolyspora* species and *Streptomyces* species.

45. The host cell of Claim 44 wherein said polyketide-producing microorganism is *Saccharopolyspora erythraea*.

46. The host cell of Claim 44 wherein said polyketide-producing microorganism is selected from the group consisting of *Streptomyces hygroscopicus*, *Streptomyces venezuelae*, and *Streptomyces caelestis*.

47. A method for altering the substrate specificity of a polyketide synthase in a first polyketide-producing microorganism comprising the steps of:

(a) isolating a first and second genomic DNA segment, each comprising a polyketide synthase wherein said first genomic DNA segment is from said first polyketide-producing microorganism and said second genomic DNA segment is from said first polyketide-producing microorganism or a second polyketide-producing microorganism;

(b) identifying one or more discrete fragments of said first genomic DNA segment, each of which encodes an acyltransferase domain;

(c) identifying one or more discrete fragments of said second genomic DNA segment, each of which encodes a related domain to said acyltransferase domain of said first genomic DNA segment; and

(d) transforming a cell of said first polyketide-producing microorganism with one or more of said fragments from step (c) under conditions suitable for the occurrence of a homologous recombination event, leading to the replacement of one or more of said fragments from said first genomic DNA segment with one or more of said fragments from step (c).

48. The method of Claim 47 wherein said first polyketide-producing microorganism is *Saccharopolyspora erythraea*.

49. The method of Claim 47 wherein said second polyketide-producing microorganism is *Streptomyces*.

50. The method of Claim 49 wherein said *Streptomyces* is selected from the group consisting of *Streptomyces antibioticus*, *Streptomyces mycarofaciens*, *Streptomyces avermitilis*, *Streptomyces hygroscopicus*, *Streptomyces caelestis*, *Streptomyces tsukubaensis*, *Streptomyces fradiae*, *Streptomyces platensis*, *Streptomyces violaceoniger*, *Streptomyces ambofaciens*, and *Streptomyces venezuelae*.

51. The method of Claim 50 wherein said *Streptomyces* is selected from the group consisting of *Streptomyces caelestis*, *Streptomyces hygroscopicus*, and *Streptomyces venezuelae*.

52. The method of Claim 47 wherein said first polyketide-producing microorganism is *Streptomyces*.

53. The method of Claim 52 wherein said *Streptomyces* is selected from the group consisting of *Streptomyces antibioticus*, *Streptomyces mycarofaciens*, *Streptomyces avermitilis*, *Streptomyces hygroscopicus*, *Streptomyces caelestis*, *Streptomyces tsukubaensis*, *Streptomyces fradiae*, *Streptomyces platensis*, *Streptomyces violaceoniger*, *Streptomyces ambofaciens*, and *Streptomyces venezuelae*.

54. The method of Claim 53 wherein said *Streptomyces* is selected from the group consisting of *Streptomyces caelestis*, *Streptomyces hygroscopicus*, and *Streptomyces venezuelae*.

55. The method of Claim 47 wherein said second polyketide-producing microorganism is *Saccharopolyspora erythraea*.

56. The method of Claim 47 wherein said related domain is selected from the group consisting of SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33 and SEQ ID NO:34.